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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/298,523 04/23/99 BRILES

D 454312-3140

EXAMINER

HM12/0228

WILLIAM S FROMMER  
FROMMER LAWRENCE & HAUG LLP  
745 FIFTH AVENUE  
NEW YORK NY 10151

MINNIEFIELD, N

ART UNIT

PAPER NUMBER

1645

DATE MAILED:

02/28/01

**Please find below and/or attached an Office communication concerning this application or proceeding.**

**Commissioner of Patents and Trademarks**



UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office

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Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/298523	04/23/99	BRILES ET AL	454312-3140

p

p

EXAMINER	
MINNIFIELD	
ART UNIT	PAPER NUMBER
1645	10

p

p

DATE MAILED:

Commissioner of Patents

Please find below a communication from the EXAMINER in charge of this application.

1. The communication filed November 11, 2000 is not fully responsive to the Office communication mailed June 19, 2000 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). **EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).**

2. Any inquiry concerning this communication or earlier communications from the examiner should be directed to N. M. Minnifield whose telephone number is (703) 305-3394. The examiner can normally be reached on Monday-Thursday from 7:00 AM-4:30 PM. The examiner can also be reached on alternate Fridays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette R. F. Smith, can be reached on (703) 308-3909. The fax phone number for TECH CENTER 1600 is (703) 308-4556.

Any inquiry of a general nature or relating to the status of this application should be directed to the TECH CENTER 1600 receptionist whose telephone number is (703) 308-0196.

N. M. Minnifield

February 27, 2001

substitute PTOL90

  
NITA MINNIFIELD  
PRIMARY EXAMINER

# Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED    CORRECTION

SERIAL NUMBER: 09/298,523A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

**RECEIVED**

NOV 28 2000

TELEPHONE 1600/2900

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid-number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                         (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
                         This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

N. Minnifield

RECEIVED Page 1 of 7  
NOV 28 2000

1645  
FILE: 021600/2900

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/298,523A  
DATE: 11/16/2000  
TIME: 18:17:02

Input Set : A:\Brilesal.app  
Output Set: N:\CRF3\11162000\I298523A.raw

Does Not Comply  
Corrected Diskette Needed

P.6

3 <110> APPLICANT: BRILES et al.  
5 <120> TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS  
6 AND STRAINS THEREOF AND USES THEREFOR  
8 <130> FILE REFERENCE: 454312-3140  
10 <140> CURRENT APPLICATION NUMBER: 09/298,523A  
11 <141> CURRENT FILING DATE: 1999-04-23  
13 <160> NUMBER OF SEQ ID NOS: 78  
15 <170> SOFTWARE: PatentIn Ver. 2.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 691  
19 <212> TYPE: PRT  
20 <213> ORGANISM: Streptococcus pneumoniae  
22 <400> SEQUENCE: 1  
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24 1 5 10 15  
26 Phe Ser Ile Gly Val Ala Ser Val Ala Val Ala Ser Leu Phe Leu Gly  
27 20 25 30  
29 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val  
30 35 40 45  
32 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu  
33 50 55 60  
35 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys  
36 65 70 75 80  
38 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile  
39 85 90 95  
41 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala  
42 100 105 110  
44 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr  
45 115 120 125  
47 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys  
48 130 135 140  
50 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu  
51 145 150 155 160  
53 Asp Gln Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys  
54 165 170 175  
56 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala  
57 180 185 190  
59 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu  
60 195 200 205  
62 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala  
63 210 215 220  
65 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys  
66 225 230 235 240  
68 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser  
69 245 250 255  
71 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu  
72 260 265 270

## RAW SEQUENCE LISTING

DATE: 11/16/2000

PATENT APPLICATION: US/09/298,523A

TIME: 18:17:02

Input Set : A:\Brilesal.app

Output Set: N:\CRF3\11162000\I298523A.raw

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NOV 28 2000

TECH CENTER 1600/2900

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74 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
75      275      280      285
77 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
78      290      295      300
80 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys
81 305      310      315      320
83 Met Leu Ser Glu Ile Gln Leu Asp Arg Arg Lys His Thr Gln Asn Val
84      325      330      335
86 Asn Leu Asn Ile Lys Leu Ser Ala Ile Lys Thr Lys Tyr Leu Tyr Glu
87      340      345      350
89 Leu Ser Val Leu Lys Glu Asn Ser Lys Lys Glu Glu Leu Thr Ser Lys
90      355      360      365
92 Thr Lys Ala Glu Leu Thr Ala Ala Phe Glu Gln Phe Lys Lys Asp Thr
93      370      375      380
95 Leu Lys Pro Glu Lys Lys Val Ala Glu Ala Glu Lys Lys Val Glu Glu
96 385      390      395      400
98 Ala Lys Lys Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr
99      405      410      415
101 Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp
102      420      425      430
104 Val Lys Val Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Asn
105      435      440      445
107 Glu Ser Arg Asn Glu Glu Lys Ile Lys Gln Ala Lys Glu Lys Val Glu
108      450      455      460
110 Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu Lys Ile Lys Thr Asp Arg
111 465      470      475      480
113 Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys
114      485      490      495
116 Lys Ala Ala Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Tyr Ala Leu
117      500      505      510
119 Glu Ala Lys Ile Ala Glu Leu Glu Tyr Glu Val Gln Arg Leu Glu Lys
120      515      520      525
122 Glu Leu Lys Glu Ile Asp Glu Ser Asp Ser Glu Asp Tyr Leu Lys Glu
123      530      535      540
125 Gly Leu Arg Ala Pro Leu Gln Ser Lys Leu Asp Thr Lys Lys Ala Lys
126 545      550      555      560
128 Leu Ser Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala
129      565      570      575
131 Glu Ile Ala Lys Leu Glu Val Gln Leu Lys Asp Ala Glu Gly Asn Asn
132      580      585      590
134 Asn Val Glu Ala Tyr Phe Lys Glu Gly Leu Glu Lys Thr Thr Ala Glu
135      595      600      605
137 Lys Lys Ala Glu Leu Glu Lys Ala Glu Ala Asp Leu Lys Lys Ala Val
138      610      615      620
140 Asp Glu Pro Glu Thr Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro
141 625      630      635      640
143 Glu Lys Pro Ala Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro
144      645      650      655
146 Ala Pro Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Ala Pro

```

RAW SEQUENCE LISTING                      DATE: 11/16/2000  
 PATENT APPLICATION:    US/09/298,523A            TIME: 18:17:02

Input Set : A:\Brilesal.app  
 Output Set: N:\CRF3\11162000\I298523A.raw

```

147          660          665          670
149 Glu Lys Pro Ala Pro Ala Pro Glu Lys Pro Ala Pro Thr Pro Glu Thr
150          675          680          685
152 Pro Lys Thr
153          690
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 707
158 <212> TYPE: PRT
159 <213> ORGANISM: Streptococcus pneumoniae
161 <400> SEQUENCE: 2
162 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
163 1 5 10 15
165 Phe Ser Ile Gly Val Ala Ser Val Ala Val Ala Ser Leu Phe Leu Gly
166 20 25 30
168 Gly Val Val His Ala Glu Gly Val Arg Ser Gly Asn Asn Leu Thr Val
169 35 40 45
171 Thr Ser Ser Gly Gln Asp Ile Ser Lys Lys Tyr Ala Asp Glu Val Glu
172 50 55 60
174 Ser His Leu Glu Ser Ile Leu Lys Asp Val Lys Lys Asn Leu Lys Lys
175 65 70 75 80
177 Val Gln His Thr Gln Asn Val Gly Leu Ile Thr Lys Leu Ser Glu Ile
178 85 90 95
180 Lys Lys Lys Tyr Leu Tyr Asp Leu Lys Val Asn Val Leu Ser Glu Ala
181 100 105 110
183 Glu Leu Thr Ser Lys Thr Lys Glu Thr Lys Glu Lys Leu Thr Ala Thr
184 115 120 125
186 Phe Glu Gln Phe Lys Lys Asp Thr Leu Pro Thr Glu Pro Glu Lys Lys
187 130 135 140
189 Val Ala Glu Ala Gln Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu
190 145 150 155 160
192 Asp Glu Lys Glu Lys Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys
193 165 170 175
195 Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala
196 180 185 190
198 Glu Leu Glu Leu Val Lys Val Lys Ala Lys Glu Ser Gln Asp Glu Glu
199 195 200 205
201 Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln Ala Glu Ala
202 210 215 220
204 Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala Lys Arg Lys
205 225 230 235 240
207 Ala Asp Ala Lys Leu Lys Glu Ala Val Glu Lys Asn Val Ala Thr Ser
208 245 250 255
210 Glu Gln Asp Lys Pro Lys Arg Arg Ala Lys Arg Gly Val Ser Gly Glu
211 260 265 270
213 Leu Ala Thr Pro Asp Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser
214 275 280 285
216 Ser Val Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu Asn Met Ala Asn
217 290 295 300
219 Glu Ser Gln Thr Glu His Arg Lys Asp Val Asp Glu Tyr Ile Lys Lys

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/298,523A

DATE: 11/16/2000  
 TIME: 18:17:02

Input Set : A:\Brilesal.app  
 Output Set: N:\CRF3\11162000\I298523A.raw

220	305					310						315				320
222	Met	Leu	Ser	Glu	Ile	Gln	Leu	Asp	Gly	Arg	Lys	His	Thr	Pro	Asn	Val
223					325						330				335	
225	Asn	Leu	Asn	Ile	Lys	Leu	Ser	Ala	Ile	Lys	Thr	Lys	Tyr	Leu	Tyr	Glu
226				340					345					350		
228	Leu	Ser	Val	Leu	Lys	Glu	Asn	Ser	Lys	Lys	Glu	Glu	Leu	Thr	Ser	Lys
229			355					360					365			
231	Thr	Lys	Ala	Glu	Leu	Thr	Ala	Ala	Phe	Glu	Gln	Phe	Lys	Lys	Asp	Thr
232		370					375					380				
234	Leu	Lys	Pro	Glu	Lys	Lys	Val	Ala	Glu	Ala	Glu	Lys	Lys	Val	Glu	Glu
235	385					390					395				400	
237	Ala	Lys	Lys	Lys	Ala	Lys	Asp	Gln	Lys	Glu	Glu	Asp	Arg	Arg	Asn	Tyr
238				405						410					415	
240	Pro	Thr	Asn	Thr	Tyr	Lys	Thr	Leu	Glu	Leu	Glu	Ile	Ala	Glu	Ser	Asp
241			420						425					430		
243	Val	Lys	Val	Lys	Glu	Ala	Glu	Leu	Glu	Leu	Val	Lys	Glu	Glu	Ala	Asn
244			435				440					445				
246	Glu	Ser	Arg	Asn	Glu	Glu	Lys	Ile	Lys	Gln	Ala	Lys	Glu	Lys	Val	Glu
247		450				455					460					
249	Ser	Lys	Lys	Ala	Glu	Ala	Thr	Arg	Leu	Glu	Lys	Ile	Lys	Thr	Asp	Arg
250	465					470					475				480	
252	Lys	Lys	Ala	Glu	Glu	Ala	Lys	Arg	Lys	Ala	Glu	Glu	Ser	Glu	Lys	
253				485					490					495		
255	Lys	Ala	Ala	Glu	Ala	Lys	Gln	Lys	Val	Asp	Ala	Glu	Glu	Tyr	Ala	Leu
256			500						505					510		
258	Glu	Ala	Lys	Ile	Ala	Glu	Leu	Glu	Tyr	Glu	Val	Gln	Arg	Leu	Glu	Lys
259		515						520					525			
261	Glu	Leu	Lys	Glu	Ile	Asp	Glu	Ser	Asp	Ser	Glu	Asp	Tyr	Leu	Lys	Glu
262		530				535					540					
264	Gly	Leu	Arg	Ala	Pro	Leu	Gln	Ser	Lys	Leu	Asp	Thr	Lys	Lys	Ala	Lys
265	545				550						555				560	
267	Leu	Ser	Lys	Leu	Glu	Leu	Ser	Asp	Lys	Ile	Asp	Glu	Leu	Asp	Ala	
268				565					570					575		
270	Glu	Ile	Ala	Lys	Leu	Glu	Val	Gln	Leu	Lys	Asp	Ala	Glu	Gly	Asn	Asn
271			580						585					590		
273	Asn	Val	Glu	Ala	Tyr	Phe	Lys	Glu	Gly	Leu	Glu	Lys	Thr	Thr	Ala	Glu
274			595					600					605			
276	Lys	Lys	Ala	Glu	Leu	Glu	Lys	Ala	Glu	Ala	Asp	Leu	Lys	Lys	Ala	Val
277		610				615						620				
279	Asp	Glu	Pro	Glu	Thr	Pro	Ala	Pro	Ala	Pro	Gln	Pro	Ala	Pro	Ala	Pro
280	625					630					635				640	
282	Glu	Lys	Pro	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Glu	Lys	Pro
283				645					650					655		
285	Ala	Pro	Ala	Pro	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Glu	Lys	Pro	Ala	Pro
286			660						665					670		
288	Ala	Pro	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Glu	Lys	Pro	Ala	Pro	Ala	Pro
289		675						680					685			
291	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Glu	Lys	Pro	Ala	Pro	Ala	Thr	Pro	Lys
292		690				695					700					

## RAW SEQUENCE LISTING

DATE: 11/16/2000

PATENT APPLICATION: US/09/298,523A

TIME: 18:17:02

Input Set : A:\Brilesal.app

Output Set: N:\CRF3\11162000\I298523A.raw

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294 Pro Glu Thr
295 705
298 <210> SEQ ID NO: 3
299 <211> LENGTH: 711
300 <212> TYPE: PRT
301 <213> ORGANISM: Streptococcus pneumoniae
303 <400> SEQUENCE: 3
304 Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
305 1 5 10 15
307 Phe Ser Ile Gly Val Ala Ser Val Val Val Ala Ser Leu Val Met Gly
308 20 25 30
310 Ser Val Val His Ala Thr Glu Asn Glu Gly Ile Thr Gln Val Ala Thr
311 35 40 45
313 Ser Tyr Asn Lys Ala Asn Glu Ser Gln Thr Glu His Arg Lys Ala Ala
314 50 55 60
316 Lys Gln Val Asp Glu Asp Ile Lys Lys Met Leu Ser Glu Ile Gln Glu
317 65 70 75 80
319 Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu Asp Lys Arg Lys His
320 85 90 95
322 Thr Gln Asn Val Asn Leu Asn Arg Lys Leu Ser Ala Ile Gln Thr Lys
323 100 105 110
325 Tyr Leu Tyr Glu Leu Arg Val Leu Lys Glu Lys Ser Lys Lys Glu Glu
326 115 120 125
328 Leu Thr Ser Lys Thr Lys Lys Glu Leu Asp Ala Ala Phe Glu Lys Phe
329 130 135 140
331 Lys Lys Glu Glu Pro Glu Leu Thr Lys Lys Leu Ala Glu Ala Lys Gln
332 145 150 155 160
334 Lys Ala Lys Ala Gln Lys Glu Glu Asp Phe Arg Asn Tyr Pro Thr Asn
335 165 170 175
337 Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Phe Asp Val Lys Val
338 180 185 190
340 Lys Glu Ala Glu Leu Glu Leu Val Lys Glu Glu Ala Lys Pro Arg Asn
341 195 200 205
343 Glu Glu Lys Ile Lys Gln Ala Lys Ala Lys Val Glu Ser Lys Lys Ala
344 210 215 220
346 Glu Ala Thr Arg Leu Glu Glu Ile Lys Thr Glu Arg Lys Lys Ala Glu
347 225 230 235 240
349 Glu Glu Ala Lys Arg Lys Ala Glu Glu Ser Glu Lys Lys Ala Ala Glu
350 245 250 255
352 Ala Lys Gln Lys Val Asp Thr Lys Glu Gln Gly Lys Pro Lys Arg Arg
353 260 265 270
355 Ala Lys Arg Gly Val Ser Gly Glu Leu Ala Thr Pro Asp Lys Lys Glu
356 275 280 285
358 Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu Thr Leu Pro
359 290 295 300
361 Ser Pro Ser Leu Asn Ala Met Ala Asn Glu Ser Gln Thr Glu His Arg
362 305 310 315 320
364 Lys Asp Val Asp Glu Tyr Ile Lys Lys Met Leu Ser Glu Ile Gln Leu
365 325 330 335

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09/298523A 6

Thr Gly Trp Leu Gln Ser Trp Tyr Tyr Leu Asn Asn Gly  
1 5 10 15  
Asp Met Ala

<210> SEQ ID NO 24

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 24

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Gly Ala Met Lys Ala  
20

<210> SEQ ID NO 25

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 25

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Gly Ala Leu Ala  
20

<210> SEQ ID NO 26

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 26

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1 5 10 15  
Val Asn

<210> SEQ ID NO 27

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 27

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1 5 10 15  
Gly Ala Met Ala  
20

<210> SEQ ID NO 28

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 28

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1 5 10 15  
Gly Ala Met Ala  
20

*see item 10 on Eva Summary Sheet*

<210> SEQ ID NO 29

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 29

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp  
1 5 10 15  
Val

<210> SEQ ID NO 30

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 30

*FYI:*

**Please Note:**

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the S quence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/298,523A

DATE: 11/16/2000

TIME: 18:17:03

Input Set : A:\Brilesal.app

Output Set: N:\CRF3\11162000\I298523A.raw

L:1664 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28  
 L:1664 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28  
 L:1664 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28  
 L:1664 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28  
 L:1664 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28  
 L:3795 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:71  
 L:3795 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:71  
 L:3795 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:71  
 L:3795 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:71  
 L:3795 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:71  
 L:3927 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:74  
 L:3927 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:74  
 L:3927 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:74  
 L:3927 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:74  
 L:3927 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:74